



032301.232.seq.ST25.txt
SEQUENCE LISTING

<11> Farwick, Mike, et al.

<12> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dep67 GENE

<13> 32301 WD 131

<14> 4

<17> Patent in version 3.1

<210> 1

<211> 1756

<212> DNA

<213> Corynebacterium glutamicum

<214>

<215> NIS

<216> (159)...(1560)

<223>

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cagatgggtg aagtagctgt gaaatgaggg gtaggggcgg gacgcgttcc agagaaagtg 180

cagatataat cagatataat cagatataat cagatataat cagatataat cagatataat 240

gagtagataa taggagga atg gaa aag cat gag gtt gtt gag aag aag gtt 241
Met Gly Lys His Glu Val Ala Gln Gln Thr Val
1 5 10

cgg ggt cct tgg cgg gaa atg gaa ggg cag cgg cgt aaa gag ttg cgg 339
Pro Gly Pro Ser Pro Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg
15 20 25

aag aag aag ggc att ggc act ggc ctg ttg att ttt gct ggc gct gta 387
Lys His Lys Ala Ile Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val
30 35 40

tat ttt att tgc cgt ttc ggg gag acc cgt cgg ggt gaa act gaa cgg 435
Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala
45 50 55

tgg gta cgt att gtg cgg gct ggg gaa gag ggc gga atg att ggc ggg 483
Trp Val Gly Ile Val Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly
60 65 70 75

tat ttc tat ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 531
Leu Ala Asp Thr Phe Ala Val Thr Ala Leu Ile Arg His Ile Leu Thr
80 85 90 95

atg cgt att cgt cat act ggg att atc cgg cgg aag aag gaa cag tta 579
Met Pro Ile Pro His Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu
100 105

682541.132.seq.ATTG.txt

ggt gag ggt tta att ggg ttt atg ggg gat aac ttc ata aat ttt gag Gly Ser Ala Leu Ser Gly Ile Val Gly Asp Asn Phe Leu Asn Ala Ser 110	677
ctc att acc aac aaa gtc tat tag ggg cgg atc cca aac ctt ggc ggu Leu Ile Thr Glu Lys Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly 115 130 135	678
gag tgg ctc gcc cag ccc gaa aac ggg gag aaa gtt tgg cgc gaa gtc Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val 140 145 150 155	723
ggc aaa ttg acc gct aat att gtg cgc gca atc gat ccc tca gat gct Gly Lys Leu Thr Ala Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala 160 165 170	771
gaa gag gtg att aac tct ggg atg atc gac aag att ggg gaa ccc acc Glu Ala Val Ile Lys Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr 175 180 185	819
ttg ggc cca cca gct ggg cgg ttg atg gaa caa ctc ctc gcc gaa gaa Trp Gly Pro Phe Ala Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala 190 195	867
aag cgg aac cag ttg tcc agc aac tgg cgc agt ggc tgc aca aaa agg Lys Pro Asn Gln Leu Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg 205 210 215	915
act tgg gct ccc gag cgg atg att gat cgc atg ctc aac cag cgc cgc Arg Trp Ala Pro Glu Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg 220 225 230 235	963
cgg att tgg cgg cgg aaa ttc act ggg cag atg gtc agc ggc aaa gtc Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val 240 245 250	1011
tat gac gag gtc ata aaa ttc act gaa gcc gtc gct gcc gat cct aac Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn 255 260 265	1059
cac gag gcc ggc aaa tcc atg ccc cca ttc ctt aat aac ttt ggc gaa His Glu Ala Arg Lys Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Ser 270 275 280	1107
gac atg cag cat gac cca ggc atg att att aaa gtt gaa gaa atc aaa Asp Leu Gln His Asp Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys 285 290 295	1155
cgg gag atc atg gcc tcc ggc gcc atc ggg caa gcc ggg cca acc atc Arg Asp Ile Met Gly Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile 300 305 310 315	1203
ttg cgg tca ccc tcc gag tgg ctc att gaa tcc gca gaa gat gag tca Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser 320 325 330	1251
tca att ccc ccc ccc aaa att tcc gaa gca gct acc agc tcc cct cca Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln 335 340 345	1299

335

340

345

aga tta att gtc gat gac tcc ctg cgg cat tca ctg gat acc cgg att 1347
 Ala Leu Leu Val Asp Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile
 335 340 345

acc gga ggc ggt ggt ttc ctg gcc gat aat tac gcc gcc gaa gtc acc 1390
 Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr
 345 350 355

ggc att ata tta gaa ttt att gaa gga ttt acc gtt gaa gaa gtt tta 1447
 Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser
 355 360 365

gag aaa atc gaa ttc atg gtc gcc aaa gac ctg caa tac atc cgc ctt 1491
 Glu Lys Ile Glu Leu Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu
 370 375 380

aat gcc aca att gta ggt gca tta gca gga ctg acc att tac gtt att 1539
 Asn Gly Thr Ile Val Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile
 385 390 395

tac cat atc ctg ttc gga ggt taactaggag taaccatcat gtcgatgca 1590
 Ser His Ile Leu Phe Gly Ala
 400 405 410

aaagacgatt ccattctgtc caagtggagc aatgcagcctt ccagctcag cagtgccgtc 1650

agtggagtag cgaagaaactt ccgtqaagaa ctctctgaga aggaagactt caacaaactt 1710

aaagacgatt ccattctgtc caagtggagc aatgcagcctt ccagctcag cagtgccgtc 1770

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<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

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Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile
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Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg
 35 40 45

Phe Val His Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
 50 55 60

Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
 65 70 75

65

75

8

Ala Val Thr Ala Ser Phe Arg His Pro Leu Tyr Leu Ser Ile Pro His
 85 90 95 100 105 110 115 120 125 130 135 140 145 150

Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
 155 160 165 170 175 180 185 190 195 200 205 210 215 220

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
 225 230 235 240 245 250 255 260 265 270 275 280 285 290

Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
 295 300 305 310 315 320 325 330 335 340 345 350 355 360

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
 365 370 375 380 385 390 395 400 405 410 415 420 425 430

Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
 435 440 445 450 455 460 465 470 475 480 485 490 495 500

Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
 505 510 515 520 525 530 535 540 545 550 555 560 565 570

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala Lys Pro Asn Gln Leu
 575 580 585 590 595 600 605 610 615 620 625 630 635 640

Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg Arg Trp Ala Pro Glu
 645 650 655 660 665 670 675 680 685 690 695 700 705 710

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
 715 720 725 730 735 740 745 750 755 760 765 770 775 780

Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
 785 790 795 800 805 810 815 820 825 830 835 840 845 850

Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
 855 860 865 870 875 880 885 890 895 900 905 910 915 920

Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
 925 930 935 940 945 950 955 960 965 970 975 980 985 990

Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060

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Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
305 310 315 320

Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
325 330 335

Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
340 345 350

Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
355 360 365

Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
370 375 380

Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
385 390 395 400

Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
405 410 415

Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
410 415 420

Gly Ala

<210> 3
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<213> Corynebacterium glutamicum

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gagutagcgc cagcctggcg tacataat 26

<210> 4
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